

QIIME analyses log - 16S

Input file paths

Sequence read filepath: 1A_read1.fastq.gz (md5: 5ad6d7a0a1cc9a94bdec84cf9ea86553)

Quality filter results

Total number of input sequences: 26114

Barcode not in mapping file: 0

Read too short after quality truncation: 105

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

1A 26009

Total number seqs written 26009

Input file paths

Sequence read filepath: 1A_read2.fastq.gz (md5: 93fe1bd1d58861c2ffc36892d12977ad)

Quality filter results

Total number of input sequences: 26114

Barcode not in mapping file: 0

Read too short after quality truncation: 252

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

1A 25862

Total number seqs written 25862

Input file paths

Sequence read filepath: 1B_read1.fastq.gz (md5: 948ed3e51f3a823d5aef104bd8121b2e)

Quality filter results

Total number of input sequences: 35417

Barcode not in mapping file: 0
Read too short after quality truncation: 161
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
1B 35256

Total number seqs written 35256

Input file paths
Sequence read filepath: 1B_read2.fastq.gz (md5: 1e5fc0afb2a8f5d142d5f6ce8336e203)
Quality filter results
Total number of input sequences: 35417
Barcode not in mapping file: 0
Read too short after quality truncation: 138
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
1B 35279

Total number seqs written 35279

Input file paths
Sequence read filepath: 1C_read1.fastq.gz (md5: a95b3286a3343a85f484fb5b5f23e2df)
Quality filter results
Total number of input sequences: 46051
Barcode not in mapping file: 0
Read too short after quality truncation: 299
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
1C 45752

Total number seqs written 45752

Input file paths

Sequence read filepath: 1C_read2.fastq.gz (md5: 4a479a4e41b2b0cfa093f48bbf6e2766)

Quality filter results

Total number of input sequences: 46051

Barcode not in mapping file: 0

Read too short after quality truncation: 261

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

1C 45790

Total number seqs written 45790

Input file paths

Sequence read filepath: 2A_read1.fastq.gz (md5: 7dd61c8382bdcd96014576e01922636d)

Quality filter results

Total number of input sequences: 37978

Barcode not in mapping file: 0

Read too short after quality truncation: 253

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2A 37725

Total number seqs written 37725

Input file paths

Sequence read filepath: 2A_read2.fastq.gz (md5: 4a64a2656410d836114e3a18d01b2e02)

Quality filter results

Total number of input sequences: 37978
Barcode not in mapping file: 0
Read too short after quality truncation: 225
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
2A 37753

Total number seqs written 37753

Input file paths
Sequence read filepath: 2B_read1.fastq.gz (md5:
b85a58d71276a77966ff8bdbcd9d8a74)

Quality filter results
Total number of input sequences: 48218
Barcode not in mapping file: 0
Read too short after quality truncation: 280
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
2B 47938

Total number seqs written 47938

Input file paths
Sequence read filepath: 2B_read2.fastq.gz (md5: ec86bb1abbf7f850efd85f1d6e14e5b9)
Quality filter results

Total number of input sequences: 48218
Barcode not in mapping file: 0
Read too short after quality truncation: 257
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2B 47961

Total number seqs written 47961

Input file paths

Sequence read filepath: 2C_read1.fastq.gz (md5:
1a5cb3ae2b6858039c14f918ad6343c1)

Quality filter results

Total number of input sequences: 45947

Barcode not in mapping file: 0

Read too short after quality truncation: 338

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2C 45609

Total number seqs written 45609

Input file paths

Sequence read filepath: 2C_read2.fastq.gz (md5:
6c692241ce50fddadac5d9c2a1e503d8)

Quality filter results

Total number of input sequences: 45947

Barcode not in mapping file: 0

Read too short after quality truncation: 305

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2C 45642

Total number seqs written 45642

Input file paths

Sequence read filepath: G1_read1.fastq.gz (md5:
c136ea509b613cc1635a788738a84db5)

Quality filter results

Total number of input sequences: 39848

Barcode not in mapping file: 0

Read too short after quality truncation: 374

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G1 39474

Total number seqs written 39474

Input file paths

Sequence read filepath: G1_read2.fastq.gz (md5:
1a8d469f05641d8635988eab3c1f1568)

Quality filter results

Total number of input sequences: 39848

Barcode not in mapping file: 0

Read too short after quality truncation: 320

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G1 39528

Total number seqs written 39528

Input file paths

Sequence read filepath: G2_read1.fastq.gz (md5: cf454b5d9a6ad1b130ffb97b8624f5c9)

Quality filter results

Total number of input sequences: 39809

Barcode not in mapping file: 0

Read too short after quality truncation: 315

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G2 39494

Total number seqs written 39494

Input file paths

Sequence read filepath: G2_read2.fastq.gz (md5: 4a70e2f5e296734ffb9670c783ca9c82)

Quality filter results

Total number of input sequences: 39809

Barcode not in mapping file: 0

Read too short after quality truncation: 258

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G2 39551

Total number seqs written 39551

Input file paths

Sequence read filepath: G3_read1.fastq.gz (md5: 6e99eeacdcd0cb1e662e8b39388e992)

Quality filter results

Total number of input sequences: 28695

Barcode not in mapping file: 0

Read too short after quality truncation: 36

Count of N characters exceeds limit: 20

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G3 28639

Total number seqs written 28639

Input file paths

Sequence read filepath: G3_read2.fastq.gz (md5:
8c1263b756ae92fc8fe8ad0029bb44ba)

Quality filter results

Total number of input sequences: 28695

Barcode not in mapping file: 0

Read too short after quality truncation: 25

Count of N characters exceeds limit: 23

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G3 28647

Total number seqs written 28647

Input file paths

Sequence read filepath: G4_read1.fastq.gz (md5:
48eb9bd7751aade5a76e1fc9a3502e27)

Quality filter results

Total number of input sequences: 24784

Barcode not in mapping file: 0

Read too short after quality truncation: 544

Count of N characters exceeds limit: 53

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G4 24187

Total number seqs written 24187

Input file paths

Sequence read filepath: G4_read2.fastq.gz (md5:
f7e260d78cb31d743b773f99ada80176)

Quality filter results

Total number of input sequences: 24784

Barcode not in mapping file: 0

Read too short after quality truncation: 551
Count of N characters exceeds limit: 33
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 300.00
G4 24200

Total number seqs written 24200

Input file paths
Sequence read filepath: G5_read1.fastq.gz (md5:
d0b8caf644345f396bda2ae1b0cf4098)

Quality filter results
Total number of input sequences: 17191
Barcode not in mapping file: 0
Read too short after quality truncation: 146
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G5 17045

Total number seqs written 17045

Input file paths
Sequence read filepath: G5_read2.fastq.gz (md5:
4049aca25d20633f1a70e6be91b2a3ae)

Quality filter results
Total number of input sequences: 17191
Barcode not in mapping file: 0
Read too short after quality truncation: 98
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00

G5 17093

Total number seqs written 17093

Input file paths

Sequence read filepath: G6_read1.fastq.gz (md5: 39b37225230b2c183139795012a731ed)

Quality filter results

Total number of input sequences: 23446

Barcode not in mapping file: 0

Read too short after quality truncation: 217

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G6 23229

Total number seqs written 23229

Input file paths

Sequence read filepath: G6_read2.fastq.gz (md5: 56ded08a83d0e214566b4484ce048173)

Quality filter results

Total number of input sequences: 23446

Barcode not in mapping file: 0

Read too short after quality truncation: 144

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G6 23302

Total number seqs written 23302

Input file paths

Sequence read filepath: G7_read1.fastq.gz (md5: 6e4fcdc08c14e5bf8a24132fc2f4ac41)

Quality filter results

Total number of input sequences: 41361

Barcode not in mapping file: 0

Read too short after quality truncation: 1271

Count of N characters exceeds limit: 30

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G7 40060

Total number seqs written 40060

Input file paths

Sequence read filepath: G7_read2.fastq.gz (md5:
90c3f56b03d5dd7bb946162044316bcc)

Quality filter results

Total number of input sequences: 41361

Barcode not in mapping file: 0

Read too short after quality truncation: 1165

Count of N characters exceeds limit: 43

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G7 40153

Total number seqs written 40153

Input file paths

Sequence read filepath: G8_read1.fastq.gz (md5:
2a9caed19b6fa44abbe9a7a03c57d31d)

Quality filter results

Total number of input sequences: 37494

Barcode not in mapping file: 0

Read too short after quality truncation: 633

Count of N characters exceeds limit: 32

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G8 36829

Total number seqs written 36829

Input file paths

Sequence read filepath: G8_read2.fastq.gz (md5:
ad686839c8b23f5d7e60ae4d37f3dd85)

Quality filter results

Total number of input sequences: 37494

Barcode not in mapping file: 0

Read too short after quality truncation: 580

Count of N characters exceeds limit: 42

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G8 36872

Total number seqs written 36872

Input file paths

Sequence read filepath: G9_read1.fastq.gz (md5:
10808c096c20989538d74d4b9f52bf6a)

Quality filter results

Total number of input sequences: 7190

Barcode not in mapping file: 0

Read too short after quality truncation: 143

Count of N characters exceeds limit: 7

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G9 7040

Total number seqs written 7040

Input file paths

Sequence read filepath: G9_read2.fastq.gz (md5:
418107ce7d48cfd142e5dac7ad4fad2d)

Quality filter results

Total number of input sequences: 7190

Barcode not in mapping file: 0

Read too short after quality truncation: 110

Count of N characters exceeds limit: 12

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G9 7068

Total number seqs written 7068

Input file paths

Sequence read filepath: V1_read1.fastq.gz (md5:
7b27af97d0dffd55b21afd024aaa4a82)

Quality filter results

Total number of input sequences: 18397

Barcode not in mapping file: 0

Read too short after quality truncation: 52

Count of N characters exceeds limit: 28

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V1 18317

Total number seqs written 18317

Input file paths

Sequence read filepath: V1_read2.fastq.gz (md5:
0f08372147e1ae771db8a01d5aa307f3)

Quality filter results

Total number of input sequences: 18397

Barcode not in mapping file: 0

Read too short after quality truncation: 59
Count of N characters exceeds limit: 16
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 300.00
V1 18322

Total number seqs written 18322

Input file paths
Sequence read filepath: V2_read1.fastq.gz (md5:
e7eaab0380317fc35b2b2a4c30e67be0)

Quality filter results
Total number of input sequences: 33288
Barcode not in mapping file: 0
Read too short after quality truncation: 2497
Count of N characters exceeds limit: 21
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V2 30770

Total number seqs written 30770

Input file paths
Sequence read filepath: V2_read2.fastq.gz (md5: a2fa88a17efa421688a163168a5c3234)
Quality filter results

Total number of input sequences: 33288
Barcode not in mapping file: 0
Read too short after quality truncation: 2495
Count of N characters exceeds limit: 28
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V2 30765

Total number seqs written 30765

Input file paths

Sequence read filepath: V3_read1.fastq.gz (md5:
37b73bda54c37dcd0756bd35dea286f9)

Quality filter results

Total number of input sequences: 59975

Barcode not in mapping file: 0

Read too short after quality truncation: 1041

Count of N characters exceeds limit: 42

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V3 58892

Total number seqs written 58892

Input file paths

Sequence read filepath: V3_read2.fastq.gz (md5:
cae2ebed09fc20519d659e0d03d9fc27)

Quality filter results

Total number of input sequences: 59975

Barcode not in mapping file: 0

Read too short after quality truncation: 1008

Count of N characters exceeds limit: 58

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V3 58909

Total number seqs written 58909

Input file paths

Sequence read filepath: V4_read1.fastq.gz (md5:
3c243e259068e022a36a780950edf0dc)

Quality filter results

Total number of input sequences: 37377

Barcode not in mapping file: 0

Read too short after quality truncation: 10046

Count of N characters exceeds limit: 22

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V4 27309

Total number seqs written 27309

Input file paths

Sequence read filepath: V4_read2.fastq.gz (md5: 63640f730f78a54357dc7b6be2f964a6)

Quality filter results

Total number of input sequences: 37377

Barcode not in mapping file: 0

Read too short after quality truncation: 10046

Count of N characters exceeds limit: 30

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V4 27301

Total number seqs written 27301

Input file paths

Sequence read filepath: V5_read1.fastq.gz (md5: 0d7fafa0640823f2a13723bd7e317ae5)

Quality filter results

Total number of input sequences: 71158

Barcode not in mapping file: 0

Read too short after quality truncation: 2486

Count of N characters exceeds limit: 50

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V5 68622

Total number seqs written 68622

Input file paths

Sequence read filepath: V5_read2.fastq.gz (md5: b3f79cee785deae01ed9a54994d93ff2)

Quality filter results

Total number of input sequences: 71158

Barcode not in mapping file: 0

Read too short after quality truncation: 2474

Count of N characters exceeds limit: 72

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V5 68612

Total number seqs written 68612

Input file paths

Sequence read filepath: V6_read1.fastq.gz (md5: c58f8670f6f65b47c565b4fe09f67d24)

Quality filter results

Total number of input sequences: 59721

Barcode not in mapping file: 0

Read too short after quality truncation: 1557

Count of N characters exceeds limit: 41

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V6 58123

Total number seqs written 58123

Input file paths

Sequence read filepath: V6_read2.fastq.gz (md5: 5439e3d7a694f5f4e6f166c6df1caf94)

Quality filter results

Total number of input sequences: 59721
Barcode not in mapping file: 0
Read too short after quality truncation: 1533
Count of N characters exceeds limit: 60
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V6 58128

Total number seqs written 58128

Input file paths

Sequence read filepath: V7_read1.fastq.gz (md5: 21cf12bd75439472cb8f8ebdc10cc923)

Quality filter results

Total number of input sequences: 61455
Barcode not in mapping file: 0
Read too short after quality truncation: 3148
Count of N characters exceeds limit: 71
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V7 58236

Total number seqs written 58236

Input file paths

Sequence read filepath: V7_read2.fastq.gz (md5:
2f4b0b7e463fbf924a581a35d695dc41)

Quality filter results

Total number of input sequences: 61455
Barcode not in mapping file: 0
Read too short after quality truncation: 3165
Count of N characters exceeds limit: 66
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V7 58224

Total number seqs written 58224

Input file paths

Sequence read filepath: V8_read1.fastq.gz (md5: 3ad6fbe8b07c8459b079b8efc2fefe4d)

Quality filter results

Total number of input sequences: 40521

Barcode not in mapping file: 0

Read too short after quality truncation: 13025

Count of N characters exceeds limit: 28

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V8 27468

Total number seqs written 27468

Input file paths

Sequence read filepath: V8_read2.fastq.gz (md5: 00a03d0b6d31f61114ee69634ffb07f3)

Quality filter results

Total number of input sequences: 40521

Barcode not in mapping file: 0

Read too short after quality truncation: 13123

Count of N characters exceeds limit: 33

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V8 27365

Total number seqs written 27365

Input file paths

Sequence read filepath: V9_read1.fastq.gz (md5: 22f58a4f014163d62e7cbcde245f0500)

Quality filter results

Total number of input sequences: 52861
Barcode not in mapping file: 0
Read too short after quality truncation: 7228
Count of N characters exceeds limit: 33
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V9 45600

Total number seqs written 45600

Input file paths

Sequence read filepath: V9_read2.fastq.gz (md5:
35202a74e3f2b7efdebf374bd3157bb3)

Quality filter results

Total number of input sequences: 52861
Barcode not in mapping file: 0
Read too short after quality truncation: 7231
Count of N characters exceeds limit: 54
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V9 45576

Total number seqs written 45576

Input file paths

Sequence read filepath: V10_read1.fastq.gz (md5:
ae1c81e744b20b2ddcd2679bf555856e)

Quality filter results

Total number of input sequences: 25933
Barcode not in mapping file: 0
Read too short after quality truncation: 151
Count of N characters exceeds limit: 51
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V10 25731

Total number seqs written 25731

Input file paths

Sequence read filepath: V10_read2.fastq.gz (md5:
53d4bd5ab69e0825f03ff21f08d310a0)

Quality filter results

Total number of input sequences: 25933

Barcode not in mapping file: 0

Read too short after quality truncation: 166

Count of N characters exceeds limit: 23

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

V10 25744

Total number seqs written 25744

Input file paths

Sequence read filepath: V11_read1.fastq.gz (md5:
bd87586f106eb7a264e72c2b312d308d)

Quality filter results

Total number of input sequences: 44167

Barcode not in mapping file: 0

Read too short after quality truncation: 1959

Count of N characters exceeds limit: 32

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V11 42176

Total number seqs written 42176

Input file paths

Sequence read filepath: V11_read2.fastq.gz (md5: 74249b1ba7f92ce2cddf753ec693ceb5)

Quality filter results

Total number of input sequences: 44167

Barcode not in mapping file: 0

Read too short after quality truncation: 1945

Count of N characters exceeds limit: 49

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V11 42173

Total number seqs written 42173

Input file paths

Sequence read filepath: V12_read1.fastq.gz (md5: ee933bf0a04fc7d837db38efe339a3e3)

Quality filter results

Total number of input sequences: 36355

Barcode not in mapping file: 0

Read too short after quality truncation: 10106

Count of N characters exceeds limit: 23

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V12 26226

Total number seqs written 26226

Input file paths

Sequence read filepath: V12_read2.fastq.gz (md5: 926858f867a8d6a999ce8470cee51bd7)

Quality filter results

Total number of input sequences: 36355

Barcode not in mapping file: 0

Read too short after quality truncation: 10275

Count of N characters exceeds limit: 31

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V12 26049

Total number seqs written 26049

qiime_config values:

pick_otus_reference_seqs_fp

/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta

sc_queue all.q

pynast_template_alignment_fp

/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-packages/qiime_default_reference/gg_13_8_otus/rep_set_aligned/85_otus.pynast.fasta

a

cluster_jobs_fp start_parallel_jobs.py

assign_taxonomy_reference_seqs_fp

/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta

torque_queue friendlyq

jobs_to_start 1

denoiser_min_per_core 50

assign_taxonomy_id_to_taxonomy_fp

/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-packages/qiime_default_reference/gg_13_8_otus/taxonomy/97_otu_taxonomy.txt

temp_dir /tmp/

blastall_fp blastall

seconds_to_sleep 1

parameter file values:

parallel:jobs_to_start 4

Input file md5 sums:

slout/seqs.fna: 6e7f1b0f24ad5a160a4e12b8c6dff13f

eztaxon_qiime_full.fasta: f574af1ce44b991a6d30123655f23602

Executing commands.

Pick Reference OTUs command

```
parallel_pick_otus_uclust_ref.py -i slout/seqs.fna -o otus//step1_otus -r  
eztaxon_qiime_full.fasta -T --jobs_to_start 4
```

Stdout:

Stderr:

Generate full failures fasta file command

```
filter_fasta.py -f slout/seqs.fna -s otus//step1_otus/seqs_failures.txt -o  
otus//step1_otus/failures.fasta
```

Stdout:

Stderr:

Executing commands.

Pick rep set command

```
pick_rep_set.py -i otus//step1_otus/seqs_otus.txt -o  
otus//step1_otus/step1_rep_set.fna -f slout/seqs.fna
```

Stdout:

Stderr:

Subsample the failures fasta file using API

```
python -c "import qiime;  
qiime.util.subsample_fasta('/home/alaricprins/16S/otus/step1_otus/failures.fasta',  
'/home/alaricprins/16S/otus/step2_otus/subsampled_failures.fasta', '0.001000')
```

"Executing commands.

Pick de novo OTUs for new clusters command

```
pick_otus.py -i otus//step2_otus//subsampled_failures.fasta -o otus//step2_otus/ -m  
uclust --denovo_otu_id_prefix New.ReferenceOTU
```

Stdout:

Stderr:

Pick representative set for subsampled failures command

```
pick_rep_set.py -i otus//step2_otus//subsamped_failures_otus.txt -o  
otus//step2_otus//step2_rep_set.fna -f otus//step2_otus//subsamped_failures.fasta
```

Stdout:

Stderr:

```
# Pick reference OTUs using de novo rep set command  
parallel_pick_otus_uclust_ref.py -i otus//step1_otus/failures.fasta -o  
otus//step3_otus/ -r otus//step2_otus//step2_rep_set.fna -T --jobs_to_start 4
```

Stdout:

Stderr:

```
# Create fasta file of step3 failures command  
filter_fasta.py -f otus//step1_otus/failures.fasta -s  
otus//step3_otus//failures_failures.txt -o otus//step3_otus//failures_failures.fasta
```

Stdout:

Stderr:

```
# Pick de novo OTUs on step3 failures command  
pick_otus.py -i otus//step3_otus//failures_failures.fasta -o otus//step4_otus/ -m uclust  
--denovo_otu_id_prefix New.CleanUp.ReferenceOTU
```

Stdout:

Stderr:

```
# Merge OTU maps command  
cat otus//step1_otus/seqs_otus.txt otus//step3_otus//failures_otus.txt  
otus//step4_otus//failures_failures_otus.txt > otus//final_otu_map.txt
```

Stdout:

Stderr:

```
# Pick representative set for subsampled failures command  
pick_rep_set.py -i otus//step4_otus//failures_failures_otus.txt -o  
otus//step4_otus//step4_rep_set.fna -f otus//step3_otus//failures_failures.fasta
```

Stdout:

Stderr:

```
# Filter singletons from the otu map using API
python -c "import qiime;
qiime.filter.filter_otus_from_otu_map('/home/alaricprins/16S/otus/final_otu_map.txt'
, '/home/alaricprins/16S/otus/final_otu_map_mc2.txt', '2')"

# Write non-singleton otus representative sequences from step1 to the final rep set
file: otus//rep_set.fna

# Copy the full input refseqs file to the new refseq file
cp eztaxon_qiime_full.fasta otus//new_refseqs.fna

# Write non-singleton otus representative sequences from step 2 and step 4 to the
final representative set and the new reference set (otus//rep_set.fna and
otus//new_refseqs.fna respectively)
```

Executing commands.

```
# Make the otu table command
make_otu_table.py -i otus//final_otu_map_mc2.txt -o otus//otu_table_mc2.biom
```

Stdout:

Stderr:

Executing commands.

```
# Assign taxonomy command
parallel_assign_taxonomy_uclust.py -i otus//rep_set.fna -o
otus//uclust_assigned_taxonomy -T --jobs_to_start 4
```

Stdout:

Stderr:

Executing commands.

```
# Add taxa to OTU table command
biom add-metadata -i otus//otu_table_mc2.biom --observation-metadata-fp
otus//uclust_assigned_taxonomy/rep_set_tax_assignments.txt -o
```

```
otus//otu_table_mc2_w_tax.biom --sc-separated taxonomy --observation-header  
OTUID,taxonomy
```

Stdout:

Stderr:

Executing commands.

```
# Align sequences command  
parallel_align_seqs_pynast.py -i otus//rep_set.fna -o otus//pynast_aligned_seqs -T --  
jobs_to_start 4
```

Stdout:

Stderr:

```
# Filter alignment command  
filter_alignment.py -o otus//pynast_aligned_seqs -i  
otus//pynast_aligned_seqs/rep_set_aligned.fasta
```

Stdout:

Stderr:

```
# Build phylogenetic tree command  
make_phylogeny.py -i otus//pynast_aligned_seqs/rep_set_aligned_pfiltered.fasta -o  
otus//rep_set.tre
```

Stdout:

Stderr:

Executing commands.

```
qiime_config values:  
pick_otus_reference_seqs_fp  
    /home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-  
packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta  
sc_queue    all.q  
pynast_template_alignment_fp  
    /home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
```

```
packages/qiime_default_reference/gg_13_8_otus/rep_set_aligned/85_otus.pynast.fast
a
cluster_jobs_fp      start_parallel_jobs.py
assign_taxonomy_reference_seqs_fp
    /home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta
torque_queue         friendlyq
jobs_to_start 1
denoiser_min_per_core 50
assign_taxonomy_id_to_taxonomy_fp
    /home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/taxonomy/97_otu_taxonomy.txt
temp_dir    /tmp/
blastall_fp  blastall
seconds_to_sleep 1
```

parameter file values:

```
parallel:jobs_to_start      1
```

Input file md5 sums:

```
otus/otu_table_mc2_w_tax_peat_16s.biom: d3810b244035a764c05825f6cd8fee2e
map_16S.txt: 717103108b9eee2684fc8a5212f246a1
otus/rep_set.tre: 2bb1d3a6bc88d40db71034c39b730730
```

Skipping 'biom summarize-table' as cdout//biom_table_summary.txt exists.

Executing commands.

```
# Filter low sequence count samples from table (minimum sequence count: 1060)
```

command

```
filter_samples_from_otu_table.py -i otus/otu_table_mc2_w_tax_peat_16s.biom -o
cdout//table_mc1060.biom -n 1060
```

Stdout:

Stderr:

```
# Rarefy the OTU table to 1060 sequences/sample command
```

```
single_rarefaction.py -i cdout//table_mc1060.biom -o cdout//table_even1060.biom -d
1060
```

Stdout:

Stderr:

Skipping beta_diversity_through_plots.py as
cdout//bdiv_even1060/weighted_unifrac_dm.txt,
cdout//bdiv_even1060/unweighted_unifrac_dm.txt exist(s).

Skipping alpha_rarefaction.py as
cdout//arare_max1060//alpha_rarefaction_plots/rarefaction_plots.html exists.

Skipping summarize_taxa_through_plots.py for as
cdout//taxa_plots/taxa_summary_plots/area_charts.html,
cdout//taxa_plots/taxa_summary_plots/bar_charts.html exist(s).

Executing commands.

```
# Collapse samples in OTU table by categories command
collapse_samples.py -m map_16S.txt -b cdout//table_mc1060.biom --output_biom_fp
cdout//taxa_plots_Site/Site_otu_table.biom --output_mapping_fp
cdout//taxa_plots_Site/Site_map.txt --collapse_fields 'Site'
```

Stdout:

Stderr:

```
# Sort OTU Table command
sort_otu_table.py -i cdout//taxa_plots_Site/Site_otu_table.biom -o
cdout//taxa_plots_Site/Site_otu_table_sorted.biom
```

Stdout:

Stderr:

```
# Summarize Taxonomy command
summarize_taxa.py -i cdout//taxa_plots_Site/Site_otu_table_sorted.biom -o
cdout//taxa_plots_Site/
```

Stdout:

Stderr:

```
# Plot Taxonomy Summary command
plot_taxa_summary.py -i
cdout//taxa_plots_Site/Site_otu_table_sorted_L2.txt,cdout//taxa_plots_Site/Site_otu_t
```

```
able_sorted_L3.txt,cdout//taxa_plots_Site/Site_otu_table_sorted_L4.txt,cdout//taxa_p  
lots_Site/Site_otu_table_sorted_L5.txt,cdout//taxa_plots_Site/Site_otu_table_sorted_  
L6.txt -o cdout//taxa_plots_Site//taxa_summary_plots/
```

Stdout:

Stderr:

```
/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-  
packages/matplotlib/collections.py:590: FutureWarning: elementwise comparison  
failed; returning scalar instead, but in the future will perform elementwise  
comparison  
if self._edgecolors == str('face'):
```

Executing commands.

```
# Collapse samples in OTU table by categories command  
collapse_samples.py -m map_16S.txt -b cdout//table_mc1060.biom --output_biom_fp  
cdout//taxa_plots_Sample/Sample_otu_table.biom --output_mapping_fp  
cdout//taxa_plots_Sample/Sample_map.txt --collapse_fields 'Sample'
```

Stdout:

Stderr:

```
# Sort OTU Table command  
sort_otu_table.py -i cdout//taxa_plots_Sample/Sample_otu_table.biom -o  
cdout//taxa_plots_Sample/Sample_otu_table_sorted.biom
```

Stdout:

Stderr:

```
# Summarize Taxonomy command  
summarize_taxa.py -i cdout//taxa_plots_Sample/Sample_otu_table_sorted.biom -o  
cdout//taxa_plots_Sample/
```

Stdout:

Stderr:

```
# Plot Taxonomy Summary command  
plot_taxa_summary.py -i  
cdout//taxa_plots_Sample/Sample_otu_table_sorted_L2.txt,cdout//taxa_plots_Sampl
```

```
e/Sample_otu_table_sorted_L3.txt,cdout//taxa_plots_Sample/Sample_otu_table_sorted_L4.txt,cdout//taxa_plots_Sample/Sample_otu_table_sorted_L5.txt,cdout//taxa_plots_Sample/Sample_otu_table_sorted_L6.txt -o cdout//taxa_plots_Sample//taxa_summary_plots/
```

Stdout:

Stderr:

```
/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-packages/matplotlib/collections.py:590: FutureWarning: elementwise comparison failed; returning scalar instead, but in the future will perform elementwise comparison
  if self._edgecolors == str('face'):
```

Executing commands.

```
# Collapse samples in OTU table by categories command
collapse_samples.py -m map_16S.txt -b cdout//table_mc1060.biom --output_biom_fp cdout//taxa_plots_Description/Description_otu_table.biom --output_mapping_fp cdout//taxa_plots_Description/Description_map.txt --collapse_fields 'Description'
```

Stdout:

Stderr:

```
# Sort OTU Table command
sort_otu_table.py -i cdout//taxa_plots_Description/Description_otu_table.biom -o cdout//taxa_plots_Description/Description_otu_table_sorted.biom
```

Stdout:

Stderr:

```
# Summarize Taxonomy command
summarize_taxa.py -i cdout//taxa_plots_Description/Description_otu_table_sorted.biom -o cdout//taxa_plots_Description/
```

Stdout:

Stderr:

```
# Plot Taxonomy Summary command
```

```
plot_taxa_summary.py -i
cdout//taxa_plots_Description/Description_otu_table_sorted_L2.txt,cdout//taxa_plots_Description/Description_otu_table_sorted_L3.txt,cdout//taxa_plots_Description/Description_otu_table_sorted_L4.txt,cdout//taxa_plots_Description/Description_otu_table_sorted_L5.txt,cdout//taxa_plots_Description/Description_otu_table_sorted_L6.txt -o cdout//taxa_plots_Description//taxa_summary_plots/
```

Stdout:

Stderr:

```
/home/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/matplotlib/collections.py:590: FutureWarning: elementwise comparison
failed; returning scalar instead, but in the future will perform elementwise
comparison
  if self._edgecolors == str('face'):
```

Skipping compressing of filtered BIOM table as cdout//table_mc1060.biom.gz exists.

Skipping compressing of rarefied BIOM table as cdout//table_even1060.biom.gz exists.

Executing commands.

```
# Boxplots (Site) command
make_distance_boxplots.py -d cdout//bdiv_even1060/weighted_unifrac_dm.txt -f
Site -o cdout//bdiv_even1060//weighted_unifrac_boxplots/ -m map_16S.txt -n 999
```

Stdout:

Stderr:

```
# Boxplots (Sample) command
make_distance_boxplots.py -d cdout//bdiv_even1060/weighted_unifrac_dm.txt -f
Sample -o cdout//bdiv_even1060//weighted_unifrac_boxplots/ -m map_16S.txt -n 999
```

Stdout:

Stderr:

```
# Boxplots (Description) command
make_distance_boxplots.py -d cdout//bdiv_even1060/weighted_unifrac_dm.txt -f
Description -o cdout//bdiv_even1060//weighted_unifrac_boxplots/ -m map_16S.txt -
n 999
```

Stdout:

Stderr:

Boxplots (Site) command

```
make_distance_boxplots.py -d cdout//bdiv_even1060/unweighted_unifrac_dm.txt -f  
Site -o cdout//bdiv_even1060/unweighted_unifrac_boxplots/ -m map_16S.txt -n 999
```

Stdout:

Stderr:

Boxplots (Sample) command

```
make_distance_boxplots.py -d cdout//bdiv_even1060/unweighted_unifrac_dm.txt -f  
Sample -o cdout//bdiv_even1060/unweighted_unifrac_boxplots/ -m map_16S.txt -n  
999
```

Stdout:

Stderr:

Boxplots (Description) command

```
make_distance_boxplots.py -d cdout//bdiv_even1060/unweighted_unifrac_dm.txt -f  
Description -o cdout//bdiv_even1060/unweighted_unifrac_boxplots/ -m  
map_16S.txt -n 999
```

Stdout:

Stderr:

Compare alpha diversity (chao1) command

```
compare_alpha_diversity.py -i cdout//arare_max1060/alpha_div_collated/chao1.txt -  
m map_16S.txt -c Site,Sample,Description -o cdout//arare_max1060/compare_chao1  
-n 999
```

Stdout:

Stderr:

Compare alpha diversity (PD_whole_tree) command

```
compare_alpha_diversity.py -i  
cdout//arare_max1060//alpha_div_collated/PD_whole_tree.txt -m map_16S.txt -c  
Site,Sample,Description -o cdout//arare_max1060//compare_PD_whole_tree -n 999
```

Stdout:

Stderr:

```
# Compare alpha diversity (observed_otus) command  
compare_alpha_diversity.py -i  
cdout//arare_max1060//alpha_div_collated/observed_otus.txt -m map_16S.txt -c  
Site,Sample,Description -o cdout//arare_max1060//compare_observed_otus -n 999
```

Stdout:

Stderr:

```
# Group significance (Site) command  
group_significance.py -i cdout//table_even1060.biom -m map_16S.txt -c Site -o  
cdout//group_significance_Site.txt
```

Stdout:

Stderr:

```
# Group significance (Sample) command  
group_significance.py -i cdout//table_even1060.biom -m map_16S.txt -c Sample -o  
cdout//group_significance_Sample.txt
```

Stdout:

Stderr:

```
# Group significance (Description) command  
group_significance.py -i cdout//table_even1060.biom -m map_16S.txt -c Description -  
o cdout//group_significance_Description.txt
```

Stdout:

Stderr:

Logging stopped at 17:31:25 on 18 Aug 2017

QIIME analyses log - ITS

Input file paths

Sequence read filepath: 1A_read1.fastq.gz (md5: 642513ea498e5bce2431bd70e7093a97)

Quality filter results

Total number of input sequences: 12421

Barcode not in mapping file: 0

Read too short after quality truncation: 902

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

1A 11519

Total number seqs written 11519

Input file paths

Sequence read filepath: 1A_read2.fastq.gz (md5: 6ba023db01ca264ed582a4f8e4628cdd)

Quality filter results

Total number of input sequences: 12421

Barcode not in mapping file: 0

Read too short after quality truncation: 830

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

1A 11591

Total number seqs written 11591

Input file paths

Sequence read filepath: 1B_read1.fastq.gz (md5: e06d5f8b298a15624363f367eb5c4767)

Quality filter results

Total number of input sequences: 4969

Barcode not in mapping file: 0

Read too short after quality truncation: 299
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
1B 4670

Total number seqs written 4670

Input file paths
Sequence read filepath: 1B_read2.fastq.gz (md5:
827187735f4cd5185b461d7d62123549)

Quality filter results
Total number of input sequences: 4969
Barcode not in mapping file: 0
Read too short after quality truncation: 287
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
1B 4682

Total number seqs written 4682

Input file paths
Sequence read filepath: 1C_read1.fastq.gz (md5: 36ff58da5d93b27e75f472ba8fdc1988)
Quality filter results

Total number of input sequences: 7132
Barcode not in mapping file: 0
Read too short after quality truncation: 563
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
1C 6569

Total number seqs written 6569

Input file paths

Sequence read filepath: 1C_read2.fastq.gz (md5: 491c978c4cedac1913a5aeabdd2992d8)

Quality filter results

Total number of input sequences: 7132

Barcode not in mapping file: 0

Read too short after quality truncation: 523

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

1C 6609

Total number seqs written 6609

Input file paths

Sequence read filepath: 2A_read1.fastq.gz (md5: a5efedecff1bc80cf77500b6127d14e5)

Quality filter results

Total number of input sequences: 136265

Barcode not in mapping file: 0

Read too short after quality truncation: 14143

Count of N characters exceeds limit: 69

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2A 122053

Total number seqs written 122053

Input file paths

Sequence read filepath: 2A_read2.fastq.gz (md5: 2868c3fc81464a5c033fc74d3d8602ab)

Quality filter results

Total number of input sequences: 136265
Barcode not in mapping file: 0
Read too short after quality truncation: 13622
Count of N characters exceeds limit: 115
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
2A 122528

Total number seqs written 122528

Input file paths
Sequence read filepath: 2B_read1.fastq.gz (md5:
34f34b2be43c5bba1ce4ec16b182a5d7)

Quality filter results
Total number of input sequences: 9959
Barcode not in mapping file: 0
Read too short after quality truncation: 1546
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
2B 8413

Total number seqs written 8413

Input file paths
Sequence read filepath: 2B_read2.fastq.gz (md5: c1283d51c375d598f39be8ac58a79daf)
Quality filter results

Total number of input sequences: 9959
Barcode not in mapping file: 0
Read too short after quality truncation: 1411
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2B 8548

Total number seqs written 8548

Input file paths

Sequence read filepath: 2C_read1.fastq.gz (md5: 5f37d50c08ac20c8c4aaaa02937dcf28)

Quality filter results

Total number of input sequences: 9068

Barcode not in mapping file: 0

Read too short after quality truncation: 152

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2C 8916

Total number seqs written 8916

Input file paths

Sequence read filepath: 2C_read2.fastq.gz (md5:

68b3b53e08549374470ec462b0f0bd2d)

Quality filter results

Total number of input sequences: 9068

Barcode not in mapping file: 0

Read too short after quality truncation: 685

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

2C 8383

Total number seqs written 8383

Input file paths

Sequence read filepath: G1_read1.fastq.gz (md5:
be640732c8f0d796228c671682b0bd62)

Quality filter results

Total number of input sequences: 80048

Barcode not in mapping file: 0

Read too short after quality truncation: 1783

Count of N characters exceeds limit: 73

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G1 78192

Total number seqs written 78192

Input file paths

Sequence read filepath: G1_read2.fastq.gz (md5:
3ab3c3011509fa476876eb38b7411289)

Quality filter results

Total number of input sequences: 80048

Barcode not in mapping file: 0

Read too short after quality truncation: 1768

Count of N characters exceeds limit: 81

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G1 78199

Total number seqs written 78199

Input file paths

Sequence read filepath: G2_read1.fastq.gz (md5:
35d7f3d381b8e7e082a216b17d9d2f0e)

Quality filter results

Total number of input sequences: 621

Barcode not in mapping file: 0

Read too short after quality truncation: 133

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G2 488

Total number seqs written 488

Input file paths
Sequence read filepath: G2_read2.fastq.gz (md5: 294c50a80c9c79c3222c6a4890203509)
Quality filter results
Total number of input sequences: 621
Barcode not in mapping file: 0
Read too short after quality truncation: 128
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G2 493

Total number seqs written 493

Input file paths
Sequence read filepath: G3_read1.fastq.gz (md5: 6e4cc3d0ebe22e0f6a55378f126396dc)
Quality filter results
Total number of input sequences: 86172
Barcode not in mapping file: 0
Read too short after quality truncation: 1235
Count of N characters exceeds limit: 64
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G3 84873

Total number seqs written 84873

Input file paths

Sequence read filepath: G3_read2.fastq.gz (md5: 414b1987893fa70afc7843554dbfbf2e)

Quality filter results

Total number of input sequences: 86172

Barcode not in mapping file: 0

Read too short after quality truncation: 1245

Count of N characters exceeds limit: 90

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G3 84837

Total number seqs written 84837

Input file paths

Sequence read filepath: G4_read1.fastq.gz (md5:

de677300b527db16d9a6c1f63d7f49e6)

Quality filter results

Total number of input sequences: 85469

Barcode not in mapping file: 0

Read too short after quality truncation: 1018

Count of N characters exceeds limit: 77

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G4 84374

Total number seqs written 84374

Input file paths

Sequence read filepath: G4_read2.fastq.gz (md5: dee50e4c901405866c08a2cef80297df)

Quality filter results

Total number of input sequences: 85469

Barcode not in mapping file: 0

Read too short after quality truncation: 1003

Count of N characters exceeds limit: 88
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G4 84378

Total number seqs written 84378

Input file paths
Sequence read filepath: G5_read1.fastq.gz (md5:
2c378add102f65810a32035b7e77d8c)
Quality filter results
Total number of input sequences: 2225
Barcode not in mapping file: 0
Read too short after quality truncation: 380
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G5 1845

Total number seqs written 1845

Input file paths
Sequence read filepath: G5_read2.fastq.gz (md5: 61d93c91e6e2c82d0a2c2f7f823ee711)
Quality filter results
Total number of input sequences: 2225
Barcode not in mapping file: 0
Read too short after quality truncation: 359
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G5 1866

Total number seqs written 1866

Input file paths

Sequence read filepath: G6_read1.fastq.gz (md5: ed1660dec1a8125e288d3ed036023d66)

Quality filter results

Total number of input sequences: 2091

Barcode not in mapping file: 0

Read too short after quality truncation: 158

Count of N characters exceeds limit: 1

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G6 1932

Total number seqs written 1932

Input file paths

Sequence read filepath: G6_read2.fastq.gz (md5: 0253ee4aff7788d51c8b7951d433aa5f)

Quality filter results

Total number of input sequences: 2091

Barcode not in mapping file: 0

Read too short after quality truncation: 171

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

G6 1920

Total number seqs written 1920

Input file paths

Sequence read filepath: G7_read1.fastq.gz (md5: ef2e3089b3592ce185be01b2fac72cf5)

Quality filter results

Total number of input sequences: 41049

Barcode not in mapping file: 0

Read too short after quality truncation: 3938
Count of N characters exceeds limit: 29
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G7 37082

Total number seqs written 37082

Input file paths
Sequence read filepath: G7_read2.fastq.gz (md5:
1c2417ab0d97f1f9aa718a33132e43d0)

Quality filter results
Total number of input sequences: 41049
Barcode not in mapping file: 0
Read too short after quality truncation: 3709
Count of N characters exceeds limit: 40
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G7 37300

Total number seqs written 37300

Input file paths
Sequence read filepath: G8_read1.fastq.gz (md5: 43f38193450a9a41a842ec1f504a3fe3)
Quality filter results

Total number of input sequences: 685
Barcode not in mapping file: 0
Read too short after quality truncation: 143
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
G8 542

Total number seqs written 542

Input file paths

Sequence read filepath: G8_read2.fastq.gz (md5:
92c2d1b32d5c93ca2a56ef0c135e52dd)

Quality filter results

Total number of input sequences: 685

Barcode not in mapping file: 0

Read too short after quality truncation: 137

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G8 548

Total number seqs written 548

Input file paths

Sequence read filepath: G9_read1.fastq.gz (md5:
9454018cf9415afb57d5180260b20759)

Quality filter results

Total number of input sequences: 70404

Barcode not in mapping file: 0

Read too short after quality truncation: 1558

Count of N characters exceeds limit: 56

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G9 68790

Total number seqs written 68790

Input file paths

Sequence read filepath: G9_read2.fastq.gz (md5:
a79a720e77beca0c31d8a72697377f75)

Quality filter results

Total number of input sequences: 70404

Barcode not in mapping file: 0

Read too short after quality truncation: 1546

Count of N characters exceeds limit: 65

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

G9 68793

Total number seqs written 68793

Input file paths

Sequence read filepath: V1_read1.fastq.gz (md5: 786062dcab125fe9a7bc9e61f29bec9e)

Quality filter results

Total number of input sequences: 28159

Barcode not in mapping file: 0

Read too short after quality truncation: 83

Count of N characters exceeds limit: 51

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V1 28025

Total number seqs written 28025

Input file paths

Sequence read filepath: V1_read2.fastq.gz (md5: c26e2480b6ff747a1dc85006af9069ea)

Quality filter results

Total number of input sequences: 28159

Barcode not in mapping file: 0

Read too short after quality truncation: 95

Count of N characters exceeds limit: 32

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

V1 28032

Total number seqs written 28032

Input file paths

Sequence read filepath: V2_read1.fastq.gz (md5:
a05102513eb8d71a494294fb8d96efb9)

Quality filter results

Total number of input sequences: 34176

Barcode not in mapping file: 0

Read too short after quality truncation: 326

Count of N characters exceeds limit: 72

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

V2 33778

Total number seqs written 33778

Input file paths

Sequence read filepath: V2_read2.fastq.gz (md5:
965a22e0e394871ee2adcc8d3d788eb5)

Quality filter results

Total number of input sequences: 34176

Barcode not in mapping file: 0

Read too short after quality truncation: 323

Count of N characters exceeds limit: 36

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

V2 33817

Total number seqs written 33817

Input file paths

Sequence read filepath: V3_read1.fastq.gz (md5:
d32435b8494cd35c511dde29e593ae5)

Quality filter results

Total number of input sequences: 2680

Barcode not in mapping file: 0

Read too short after quality truncation: 110

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V3 2570

Total number seqs written 2570

Input file paths

Sequence read filepath: V3_read2.fastq.gz (md5:
63e3d816a622cf0d23a263ab0e331d6d)

Quality filter results

Total number of input sequences: 2680

Barcode not in mapping file: 0

Read too short after quality truncation: 116

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V3 2564

Total number seqs written 2564

Input file paths

Sequence read filepath: V5_read1.fastq.gz (md5:
095008b6327cd393fb9d11637572f436)

Quality filter results

Total number of input sequences: 5669

Barcode not in mapping file: 0

Read too short after quality truncation: 349

Count of N characters exceeds limit: 0

Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V5 5320

Total number seqs written 5320

Input file paths
Sequence read filepath: V5_read2.fastq.gz (md5: 6badc2cc451f83ca82aabf8260a332fa)
Quality filter results
Total number of input sequences: 5669
Barcode not in mapping file: 0
Read too short after quality truncation: 338
Count of N characters exceeds limit: 0
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V5 5331

Total number seqs written 5331

Input file paths
Sequence read filepath: V6_read1.fastq.gz (md5: c8e0c4b6817902fecb0cec3bef0c76f3)
Quality filter results
Total number of input sequences: 66521
Barcode not in mapping file: 0
Read too short after quality truncation: 9258
Count of N characters exceeds limit: 38
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V6 57225

Total number seqs written 57225

Input file paths

Sequence read filepath: V6_read2.fastq.gz (md5:
fc9709f5017f46a359d5030d7030b3d4)

Quality filter results

Total number of input sequences: 66521

Barcode not in mapping file: 0

Read too short after quality truncation: 9310

Count of N characters exceeds limit: 57

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V6 57154

Total number seqs written 57154

Input file paths

Sequence read filepath: V7_read1.fastq.gz (md5:
4b3f4ead15ab51d811a481604894608a)

Quality filter results

Total number of input sequences: 77662

Barcode not in mapping file: 0

Read too short after quality truncation: 36198

Count of N characters exceeds limit: 25

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

V7 41439

Total number seqs written 41439

Input file paths

Sequence read filepath: V7_read2.fastq.gz (md5:
d0078bdd730ee3036abdb00bc028167b)

Quality filter results

Total number of input sequences: 77662

Barcode not in mapping file: 0

Read too short after quality truncation: 36043
Count of N characters exceeds limit: 51
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 300.00
V7 41568

Total number seqs written 41568

Input file paths
Sequence read filepath: V9_read1.fastq.gz (md5:
410ddf1b69f30149b304c9710d5a9c62)

Quality filter results
Total number of input sequences: 72267
Barcode not in mapping file: 0
Read too short after quality truncation: 14384
Count of N characters exceeds limit: 40
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 176.00
V9 57843

Total number seqs written 57843

Input file paths
Sequence read filepath: V9_read2.fastq.gz (md5: 23b5b5ebc84a5fcc713e5e8f08a19de2)
Quality filter results

Total number of input sequences: 72267
Barcode not in mapping file: 0
Read too short after quality truncation: 43170
Count of N characters exceeds limit: 27
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 300.00
V9 29070

Total number seqs written 29070

Input file paths

Sequence read filepath: V10_read1.fastq.gz (md5: cf3eae1a91468a99cff7c0e5e7265f3d)

Quality filter results

Total number of input sequences: 10541

Barcode not in mapping file: 0

Read too short after quality truncation: 25

Count of N characters exceeds limit: 22

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 301.00

V10 10494

Total number seqs written 10494

Input file paths

Sequence read filepath: V10_read2.fastq.gz (md5: 03ebca1fae89b6dec767bd9ad73e08d2)

Quality filter results

Total number of input sequences: 10541

Barcode not in mapping file: 0

Read too short after quality truncation: 26

Count of N characters exceeds limit: 19

Illumina quality digit = 0: 0

Barcode errors exceed max: 0

Result summary (after quality filtering)

Median sequence length: 300.00

V10 10496

Total number seqs written 10496

Input file paths

Sequence read filepath: V11_read1.fastq.gz (md5: abc995ca4fd81dc3dce2c22cade8d5f4)

Quality filter results

Total number of input sequences: 158694
Barcode not in mapping file: 0
Read too short after quality truncation: 15957
Count of N characters exceeds limit: 113
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 300.00
V11 142624

Total number seqs written 142624

Input file paths

Sequence read filepath: V11_read2.fastq.gz (md5:
720ef1696bbd5970cd0a7d0733c362cc)

Quality filter results

Total number of input sequences: 158694
Barcode not in mapping file: 0
Read too short after quality truncation: 15800
Count of N characters exceeds limit: 132
Illumina quality digit = 0: 0
Barcode errors exceed max: 0

Result summary (after quality filtering)
Median sequence length: 301.00
V11 142762

Total number seqs written 142762

qiime_config values:

pick_otus_reference_seqs_fp

/Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta
sc_queue all.q

pynast_template_alignment_fp

/Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set_aligned/85_otus.pynast.fast
a

cluster_jobs_fp start_parallel_jobs.py

```
assign_taxonomy_reference_seqs_fp
    /Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta
torque_queue      friendlyq
jobs_to_start 1
denoiser_min_per_core 50
assign_taxonomy_id_to_taxonomy_fp
    /Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/taxonomy/97_otu_taxonomy.txt
temp_dir    /var/folders/fp/n478ts1n2ps67vp0g30046tr0000gn/T/
blastall_fp  blastall
seconds_to_sleep 1
```

parameter file values:

```
assign_taxonomy:reference_seqs_fp    its_12_11_otus/rep_set/97_otus.fasta
assign_taxonomy:id_to_taxonomy_fp
    its_12_11_otus/taxonomy/97_otu_taxonomy.txt
assign_taxonomy:assignment_method  blast
parallel;jobs_to_start      1
pick_otus:enable_rev_strand_match  True
```

Input file md5 sums:

```
slout/seqs.fna: 857b0cec48aecf02df63bab57e288f86
its_12_11_otus/rep_set/97_otus.fasta: 43064e49574c847df9e03acfc7115e02
```

Forcing --suppress_new_clusters as this is reference-based OTU picking.

Executing commands.

Pick Reference OTUs command

```
pick_otus.py -i slout/seqs.fna -o otus//step1_otus -r
its_12_11_otus/rep_set/97_otus.fasta -m uclust_ref --enable_rev_strand_match --
suppress_new_clusters
```

Stdout:

Stderr:

Generate full failures fasta file command

```
filter_fasta.py -f slout/seqs.fna -s otus//step1_otus/seqs_failures.txt -o
otus//step1_otus/failures.fasta
```

Stdout:

Stderr:

Executing commands.

```
# Pick rep set command
pick_rep_set.py -i otus//step1_otus/seqs_otus.txt -o
otus//step1_otus/step1_rep_set.fna -f slout/seqs.fna
```

Stdout:

Stderr:

```
# Subsample the failures fasta file using API
python -c "import qiime;
qiime.util.subsample_fasta('/Users/alaricprins/ITS/otus/step1_otus/failures.fasta',
'/Users/alaricprins/ITS/otus/step2_otus/subsampled_failures.fasta', '0.001000')
```

"Forcing --suppress_new_clusters as this is reference-based OTU picking.

Executing commands.

```
# Pick de novo OTUs for new clusters command
pick_otus.py -i otus//step2_otus//subsampled_failures.fasta -o otus//step2_otus/ -m
uclust --denovo_otu_id_prefix New.ReferenceOTU --enable_rev_strand_match
```

Stdout:

Stderr:

```
# Pick representative set for subsampled failures command
pick_rep_set.py -i otus//step2_otus//subsampled_failures_otus.txt -o
otus//step2_otus//step2_rep_set.fna -f otus//step2_otus//subsampled_failures.fasta
```

Stdout:

Stderr:

```
# Pick reference OTUs using de novo rep set command
pick_otus.py -i otus//step1_otus/failures.fasta -o otus//step3_otus/ -r
otus//step2_otus//step2_rep_set.fna -m uclust_ref --enable_rev_strand_match --
suppress_new_clusters
```

Stdout:

Stderr:

```
# Create fasta file of step3 failures command
filter_fasta.py -f otus//step1_otus/failures.fasta -s
otus//step3_otus//failures_failures.txt -o otus//step3_otus//failures_failures.fasta
```

Stdout:

Stderr:

```
# Pick de novo OTUs on step3 failures command
pick_otus.py -i otus//step3_otus//failures_failures.fasta -o otus//step4_otus/ -m uclust
--denovo_otu_id_prefix New.CleanUp.ReferenceOTU --enable_rev_strand_match
```

Stdout:

Stderr:

```
# Merge OTU maps command
cat otus//step1_otus/seqs_otus.txt otus//step3_otus//failures_otus.txt
otus//step4_otus//failures_failures_otus.txt > otus//final_otu_map.txt
```

Stdout:

Stderr:

```
# Pick representative set for subsampled failures command
pick_rep_set.py -i otus//step4_otus//failures_failures_otus.txt -o
otus//step4_otus//step4_rep_set.fna -f otus//step3_otus//failures_failures.fasta
```

Stdout:

Stderr:

```
# Filter singletons from the otu map using API
python -c "import qiime;
qiime.filter.filter_otus_from_otu_map('/Users/alaricprins/ITS/otus/final_otu_map.txt'
, '/Users/alaricprins/ITS/otus/final_otu_map_mc2.txt', '2')"
```

```
# Write non-singleton otus representative sequences from step1 to the final rep set
file: otus//rep_set.fna
```

```
# Copy the full input refseqs file to the new refseq file
cp its_12_11_otus/rep_set/97_otus.fasta otus//new_refseqs.fna
```

```
# Write non-singleton otus representative sequences from step 2 and step 4 to the
final representative set and the new reference set (otus//rep_set.fna and
otus//new_refseqs.fna respectively)
```

Executing commands.

```
# Make the otu table command
make_otu_table.py -i otus//final_otu_map_mc2.txt -o otus//otu_table_mc2.biom
```

Stdout:

Stderr:

Executing commands.

```
# Assign taxonomy command
assign_taxonomy.py -o otus//blast_assigned_taxonomy -i otus//rep_set.fna --
reference_seqs_fp its_12_11_otus/rep_set/97_otus.fasta --id_to_taxonomy_fp
its_12_11_otus/taxonomy/97_otu_taxonomy.txt --assignment_method blast
```

Stdout:

Stderr:

Executing commands.

```
# Add taxa to OTU table command
biom add-metadata -i otus//otu_table_mc2.biom --observation-metadata-fp
otus//blast_assigned_taxonomy/rep_set_tax_assignments.txt -o
otus//otu_table_mc2_w_tax.biom --sc-separated taxonomy --observation-header
OTUID,taxonomy
```

Stdout:

Stderr:

qiime_config values:

```

pick_otus_reference_seqs_fp
    /Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta
sc_queue    all.q
pynast_template_alignment_fp
    /Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set_aligned/85_otus.pynast.fast
a
cluster_jobs_fp    start_parallel_jobs.py
assign_taxonomy_reference_seqs_fp
    /Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/rep_set/97_otus.fasta
torque_queue    friendlyq
jobs_to_start 1
denoiser_min_per_core    50
assign_taxonomy_id_to_taxonomy_fp
    /Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/qiime_default_reference/gg_13_8_otus/taxonomy/97_otu_taxonomy.txt
temp_dir    /var/folders/fp/n478ts1n2ps67vp0g30046tr0000gn/T/
blastall_fp    blastall
seconds_to_sleep    1

```

parameter file values:

```

beta_diversity:metrics    bray_curtis
alpha_diversity:metrics    observed_otus,chao1
parallel:jobs_to_start    1

```

Input file md5 sums:

```

otus/otu_table_mc2_w_tax.biom: 1cebd45b8cf5723e45dd8ef8b1f8de47
map_ITS.txt: 1a75c6b910018029f133843f30a5ae37

```

Executing commands.

```

# Generate BIOM table summary command
biom summarize-table -i otus/otu_table_mc2_w_tax.biom -o
cdout//biom_table_summary.txt

```

Stdout:

Stderr:

```

# Filter low sequence count samples from table (minimum sequence count: 160)
command

```

```
filter_samples_from_otu_table.py -i otus/otu_table_mc2_w_tax.biom -o  
cdout//table_mc160.biom -n 160
```

Stdout:

Stderr:

```
# Rarefy the OTU table to 160 sequences/sample command  
single_rarefaction.py -i cdout//table_mc160.biom -o cdout//table_even160.biom -d  
160
```

Stdout:

Stderr:

Executing commands.

```
# Beta Diversity (bray_curtis) command  
beta_diversity.py -i cdout//table_even160.biom -o cdout//bdiv_even160/ --metrics  
bray_curtis
```

Stdout:

Stderr:

```
/Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-  
packages/numpy/core/fromnumeric.py:2645: VisibleDeprecationWarning: `rank` is  
deprecated; use the `ndim` attribute or function instead. To find the rank of a matrix  
see `numpy.linalg.matrix_rank`.  
VisibleDeprecationWarning)
```

```
# Rename distance matrix (bray_curtis) command  
mv cdout//bdiv_even160//bray_curtis_table_even160.txt  
cdout//bdiv_even160//bray_curtis_dm.txt
```

Stdout:

Stderr:

```
# Principal coordinates (bray_curtis) command  
principal_coordinates.py -i cdout//bdiv_even160//bray_curtis_dm.txt -o  
cdout//bdiv_even160//bray_curtis_pc.txt
```

Stdout:

Stderr:

```
# Make emperor plots, bray_curtis) command
make_emperor.py -i cdout//bdiv_even160//bray_curtis_pc.txt -o
cdout//bdiv_even160//bray_curtis_emperor_pcoa_plot/ -m map_ITS.txt
```

Stdout:

Stderr:

Executing commands.

```
# Alpha rarefaction command
multiple_rarefactions.py -i cdout//table_mc160.biom -m 10 -x 160 -s 15 -o
cdout//arare_max160//rarefaction/
```

Stdout:

Stderr:

```
# Alpha diversity on rarefied OTU tables command
alpha_diversity.py -i cdout//arare_max160//rarefaction/ -o
cdout//arare_max160//alpha_div/ --metrics observed_otus,chao1
```

Stdout:

Stderr:

```
# Collate alpha command
collate_alpha.py -i cdout//arare_max160//alpha_div/ -o
cdout//arare_max160//alpha_div_collated/
```

Stdout:

Stderr:

```
# Removing intermediate files command
rm -r cdout//arare_max160//rarefaction/ cdout//arare_max160//alpha_div/
```

Stdout:

Stderr:

```
# Rarefaction plot: All metrics command
make_rarefaction_plots.py -i cdout//arare_max160//alpha_div_collated/ -m
map_ITS.txt -o cdout//arare_max160//alpha_rarefaction_plots/
```

Stdout:

Stderr:

```
/Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-
packages/matplotlib/collections.py:590: FutureWarning: elementwise comparison
failed; returning scalar instead, but in the future will perform elementwise
comparison
  if self._edgecolors == str('face'):
```

Skipping compare_alpha_diversity.py as no categories were provided.

Executing commands.

```
# Sort OTU Table command
sort_otu_table.py -i cdout//table_mc160.biom -o
cdout//taxa_plots/table_mc160_sorted.biom
```

Stdout:

Stderr:

```
# Summarize Taxonomy command
summarize_taxa.py -i cdout//taxa_plots/table_mc160_sorted.biom -o
cdout//taxa_plots/
```

Stdout:

Stderr:

```
# Plot Taxonomy Summary command
plot_taxa_summary.py -i
cdout//taxa_plots/table_mc160_sorted_L2.txt,cdout//taxa_plots/table_mc160_sorted_
L3.txt,cdout//taxa_plots/table_mc160_sorted_L4.txt,cdout//taxa_plots/table_mc160_s
orted_L5.txt,cdout//taxa_plots/table_mc160_sorted_L6.txt -o
cdout//taxa_plots//taxa_summary_plots/
```

Stdout:

Stderr:

```
/Users/alaricprins/miniconda3/envs/qiime1/lib/python2.7/site-  
packages/matplotlib/collections.py:590: FutureWarning: elementwise comparison  
failed; returning scalar instead, but in the future will perform elementwise  
comparison
```

```
if self._edgecolors == str('face'):
```

Executing commands.

```
# Compress the filtered BIOM table command  
gzip cdout//table_mc160.biom
```

Stdout:

Stderr:

```
# Compress the rarefied BIOM table command  
gzip cdout//table_even160.biom
```

Stdout:

Stderr:

Logging stopped at 15:01:45 on 19 Aug 2017